














## Sequences producing significant alignments:

Score E  
(bits) Value

gi 13899257 ref NP_113622.1	chromosome 7 open reading fram...	728	0.0	
gi 11967945 ref NP_071863.1	hypothetical protein, clone 1-...	633	e-180	
gi 38454298 ref NP_942076.1	Unknown (protein for MGC:72996...	515	c-144	
gi 40807187 gb AAH65312.1	Unknown (protein for MGC:77146) ...	225	3e-57	
gi 38091832 ref XP_126502.2	RIKEN cDNA 2010008E23 [Mus mus...	158	4e-37	
gi 16740606 gb AAH16187.1	RIKEN cDNA 2010008E23 gene [Mus ...	158	4e-37	
gi 20988715 gb AAH29841.1	2010008E23Rik protein [Mus muscu...	158	4e-37	
gi 12842172 dbj BAB25500.1	unnamed protein product [Mus mu...	151	3e-35	
gi 28973799 ref NP_803190.1	hypothetical protein MGC3123 [...	151	4e-35	
gi 33341676 gb AAQ15209.1	FP2653 [Homo sapiens] >gi 371826...	151	4e-35	
gi 27689889 ref XP_221010.1	similar to RIKEN cDNA 2010008E...	144	5e-33	
gi 22204247 emb CAD43429.1	SI:dZ180G5.5 (novel ubiquitin) ...	108	2e-22	
gi 10433006 dbj BAB13886.1	unnamed protein product [Homo s...	68	4e-10	
gi 283528 pir S27786	acidic protein - Caenorhabditis eleg...	55	3e-06	
gi 17551804 ref NP_498916.1	ubiquitin domain containing pr...	55	3e-06	
gi 39585075 emb CAE62726.1	Hypothetical protein CBG06886 [...	54	7e-06	
gi 13129118 ref NP_077012.1	hypothetical protein MGC3123 [...	47	0.001	
gi 41616494 tpq DAA03341.1	TPA: HDC18999 [Drosophila melan...	45	0.005	
gi 30348407 emb CAC84278.1	stpC [Saimiriine herpesvirus 2]...	44	0.008	
gi 38174711 gb AAH61325.1	MGC75814 protein [Xenopus tropic...	43	0.015	

gi 17384405 emb CAD13245.1	bA113024.1 (similar to insulin-...	43	0.015	
gi 30348416 emb CAC84992.1	saimiri transformation-associat...	43	0.020	
gi 41616370 tpg DAA03279.1	TPA: HDC18148 [Drosophila melan...	43	0.020	
gi 1743279 emb CAA67869.1	StpC139 [Saimiriine herpesvirus 2]	43	0.020	
gi 41617660 tpg DAA02769.1	TPA: HDC08319 [Drosophila melan...	42	0.027	
gi 9256600 ref NP_061722.1	protocadherin alpha subfamily C...	42	0.027	
gi 14165431 ref NP_114089.1	protocadherin alpha subfamily ...	42	0.027	
gi 43107036 gb EAC19557.1	unknown [environmental sequence]	42	0.027	
gi 41327160 ref NP_898828.1	trinucleotide repeat containin...	42	0.027	
gi 16933557 ref NP_003728.1	protocadherin 16 precursor; fi...	42	0.027	
gi 2565063 gb AAB91442.1	CTG4a [Homo sapiens]	42	0.027	
gi 38648766 gb AAH63288.1	PCDHAC2 protein [Homo sapiens]	42	0.027	
gi 43693587 gb EAF02012.1	unknown [environmental sequence]	42	0.027	
gi 33942072 ref NP_006577.2	trinucleotide repeat containin...	42	0.027	
gi 43203317 gb EAC67209.1	unknown [environmental sequence]	42	0.036	
gi 30354634 gb AAH51836.1	LRP8 protein [Homo sapiens]	42	0.036	
gi 34865759 ref XP_243524.2	similar to lipoprotein recepto...	41	0.049	
gi 15825005 gb AAL09566.1	lipoprotein receptor-related pro...	41	0.049	
gi 6678720 ref NP_032538.1	low density lipoprotein recepto...	41	0.049	
gi 300162 gb AAB26494.1	alpha-2-macroglobulin receptor, A2...	41	0.049	
gi 26349007 dbj EAC38143.1	unnamed protein product [Mus mu...	41	0.049	
gi 27881830 gb AAH43675.1	Lrp1 protein [Mus musculus]	41	0.049	
gi 15825096 gb AAL09567.1	lipoprotein receptor-related pro...	41	0.049	
gi 15529624 gb AAL01375.1	PTPRE [Homo sapiens]	41	0.066	
gi 5729993 ref NP_006495.1	protein tyrosine phosphatase, r...	41	0.066	
gi 32405458 ref XP_323342.1	predicted protein [Neurospora ...	41	0.066	
gi 116896 sp P22576 COLL SHV2C	Collagen-like protein >gi 93...	41	0.088	
gi 30348404 emb CAC84986.1	saimiri transformation-associat...	41	0.088	
gi 21166382 ref NP_620063.1	neurexin 2 isoform beta precu...	41	0.088	
gi 1743282 emb CAA67871.1	StpC484 [Saimiriine herpesvirus 2]	41	0.088	
gi 4758686 ref NP_002323.1	low density lipoprotein-related...	40	0.12	
gi 28379108 ref NP_786000.1	integral membrane protein [Lac...	40	0.12	
gi 17028418 gb AAH17526.1	Tnfrsf25 protein [Mus musculus]	40	0.16	
gi 14279974 gb AAK58831.1	lysophosphatidic acid acyltransf...	40	0.16	
gi 17975768 ref NP_004434.2	ephrin receptor EphB3 precurs...	40	0.16	
gi 41617130 tpg DAA02504.1	TPA: HDC06391 [Drosophila melan...	40	0.16	
gi 14279976 gb AAK58832.1	lysophosphatidic acid acyltransf...	40	0.16	
gi 32407261 ref XP_324215.1	predicted protein [Neurospora ...	40	0.16	
gi 4758688 ref NP_004622.1	low density lipoprotein recepto...	40	0.16	
gi 1708164 sp P54753 EPB3 HUMAN	Ephrin type-B receptor 3 pr...	40	0.16	
gi 15451868 ref NP_150643.1	low density lipoprotein recept...	40	0.16	
gi 15451866 ref NP_059992.2	low density lipoprotein recept...	40	0.16	
gi 41386737 ref NP_803484.1	1-acylglycerol-3-phosphate O-a...	40	0.16	
gi 1834534 emb CAA99509.1	apolipoprotein E receptor 2 906 ...	40	0.16	
gi 43873036 gb EAF90508.1	unknown [environmental sequence]	39	0.21	
gi 23463263 ref NP_695206.1	prepro-Neuropeptide W polypept...	39	0.21	
gi 44580550 gb EAK25059.1	unknown [environmental sequence]	39	0.21	
gi 38512117 gb AAH61796.1	Adam15 protein [Rattus norvegicus]	39	0.21	
gi 34877564 ref XP_214295.2	similar to hypothetical protei...	39	0.21	
gi 41617360 tpg DAA02619.1	TPA: HDC07244 [Drosophila melan...	39	0.21	








gi 9945328 ref NP_064704.1	a disintegrin and metalloprotei...	39	0.21	
gi 33355652 gb AAQ16195.1	latent membrane protein 1 [Human...	39	0.21	
gi 43032543 gb EAB82911.1	unknown [environmental sequence]	39	0.21	
gi 43287536 gb EAD09607.1	unknown [environmental sequence]	39	0.21	
gi 43732193 gb EAF20863.1	unknown [environmental sequence]	39	0.21	
gi 13236579 ref NP_077306.1	solute carrier family 27 membe...	39	0.29	
gi 24642080 ref NP_727818.1	CG32594-PD [Drosophila melanog...	39	0.29	
gi 5441942 gb AAD43187.1	supported by mouse EST AA538043 (...)	39	0.29	
gi 28870062 ref NP_792681.1	conserved hypothetical protein...	39	0.29	
gi 16763443 ref NP_459058.1	putative transcriptional regul...	39	0.29	
gi 14042219 dbj BAB55156.1	unnamed protein product [Homo s...	39	0.29	
gi 346951 pir A44399	stromelysin 3 (EC 3.4.24.-) - mouse	39	0.29	
gi 23471875 ref ZP_00127203.1	COG2304: Uncharacterized pro...	39	0.29	
gi 18676616 dbj BAB84960.1	FLJ00207 protein [Homo sapiens]	39	0.29	
gi 42662491 ref XP_117224.5	similar to RIKEN cDNA 0610009J...	39	0.29	
gi 13385766 ref NP_080533.1	socius [Mus musculus] >gi 1285...	39	0.29	
gi 7715870 gb AAF68173.1	mannose 6-phosphate/insulin-like ...	39	0.29	
gi 34531084 dbj BAC86050.1	unnamed protein product [Homo s...	39	0.29	
gi 26339360 dbj BAC33351.1	unnamed protein product [Mus mu...	39	0.29	
gi 34852277 ref XP_215351.2	similar to cysteine-rich prote...	39	0.29	
gi 23104640 ref ZP_00091102.1	hypothetical protein [Azotob...	38	0.51	
gi 6678894 ref NP_032632.1	matrix metalloproteinase 11; st...	38	0.51	
gi 31543531 ref NP_035342.2	protein tyrosine phosphatase, ...	38	0.51	
gi 2507226 sp P49446 PTPE MOUSE	Protein-tyrosine phosphatas...	38	0.51	
gi 33355648 gb AAQ16193.1	latent membrane protein 1 [Human...	38	0.51	
gi 41619762 tpg DAA04313.1	TPA: HDC15396 [Drosophila melan...	38	0.51	
gi 7439344 pir JC6132	protein-tyrosine-phosphatase (EC 3.1...	38	0.51	
gi 4406172 gb AAD19887.1	latent membrane protein-1 [Human ...]	38	0.51	
gi 7435843 pir JC6197	stromelysin 3 (EC 3.4.24.-) - rat	38	0.51	
gi 38374134 gb AAR19270.1	latent membrane protein 1 [Human...	38	0.51	

## Alignments

Get selected sequences

Select all

Deselect all

 >gi|13899257|ref|NP\_113622.1|  chromosome 7 open reading frame 21 [Homo sapiens]  
gi|34922062|sp|Q9BVT8|CG21\_HUMAN  Protein C7orf21 (SB144)  
gi|12654233|gb|AAH00936.1|  C7orf21 protein [Homo sapiens]  
gi|21303411|gb|AAK67645.1|  hypothetical membrane protein SB144 precursor [Homo s...]  
gi|21620058|gb|AAH33182.1|  Chromosome 7 open reading frame 21 [Homo sapiens]  
gi|37182085|gb|AAQ88845.1|  TLIE763 [Homo sapiens]

Length = 246

Score = 728 bits (1709), Expect = 0.0

Identities = 236/245 (96%), Positives = 236/245 (96%), Gaps = 5/245 (2%)

Query: 1 TLIEGVGDEVTVLFVSLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSMTM--TDS 58

TLIEGVGDEVTVLFVSLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPS M TDS

Sbjct: 2 TLIEGVGDEVTVLFVSLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDS 61

Query: 59 MRGEAPGAETPSLRHRGQM-QPEPSTGFTATPPAPDSPQEPLVRLKFLNDSEQVAM-WP 116

MRGEAPGAETPSLRHRGQ QPEPSTGFTATPPAPDSPQEPLVLRKFLNDSEQVA WP  
 Sbjct: 62 MRGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRKFLNDSEQVARAWP 121

Query: 117 HDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPP 176  
 HDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPP  
 Sbjct: 122 HDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPP 181

Query: 177 CPPGSEPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAF 236  
 CPPGSEPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAF  
 Sbjct: 182 CPPGSEPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAF 241

Query: 237 -MYRP 240  
 MYRP  
 Sbjct: 242 AMYRP 246

[>gi|11967945|ref|NP\_071863.1|] [ ] hypothetical protein, clone 1-2 [Mus musculus]  
 gi|34922148|sp|Q9JMG3|CG21 MOUSE [ ] Protein C7orf21 homolog  
 gi|7259236|dbj|BAA92747.1| [ ] contains transmembrane (TM) region [Mus musculus]  
 gi|12842088|dbj|BAB25465.1| [ ] unnamed protein product [Mus musculus]  
 gi|18043424|gb|AAH19547.1| [ ] Hypothetical protein, clone 1-2 [Mus musculus]  
 Length = 245

Score = 633 bits (1487), Expect = e-180  
 Identities = 213/244 (87%), Positives = 222/244 (90%), Gaps = 6/244 (2%)

Query: 2 LIEGVGDEVTVLFVLAALLVLAALAWVSTHTAEGGDPLPQPSGTPTPSQPS--MMMTDSM 59  
 LIEGVGDEVTVLF+VLAALLVLAALAWVSTHT E DP PQP GT TP+QPS M +DS+  
 Sbjct: 3 LIEGVGDEVTVLF+VLAALLVLAALAWVSTHTTESTDPQPQPPGTTTPAQPSSEAMSASDSI 62

Query: 60 RGEAPGAETPSLRHRGQM-QPEPSTGFTATPPAPDSPQEPLVLRKFLNDSEQVAM-WPH 117  
 R EAPGAE+PSLRHRG QPEP TG TA+ P PDSPQEPL+LRLKFLNDSEQVA WP  
 Sbjct: 63 REEAPGAESPRLRHRGPSAQPEPDTGVTASTP-PDSPQEPLLLRLKFLNDSEQVARAWPQ 121

Query: 118 DTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPPC 177  
 DTIGSLKRTQFPGE+EQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPP+PPC  
 Sbjct: 122 DTIGSLKRTQFPGEQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPHPPC 181

Query: 178 PPGSEPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAF- 236  
 PPGSEPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAF  
 Sbjct: 182 PPGSEPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAFA 241

Query: 237 MYRP 240  
 MYRP  
 Sbjct: 242 MYRP 245

[>gi|38454298|ref|NP\_942076.1|] [ ] Unknown (protein for MGC:72996) [Rattus norvegicus]  
 gi|37589846|gb|AAH59162.1| [ ] Unknown (protein for MGC:72996) [Rattus norvegicus]  
 Length = 190

Score = 515 bits (1207), Expect = e-144  
 Identities = 171/191 (89%), Positives = 176/191 (92%), Gaps = 6/191 (3%)

Query: 55 MT--DSMRGEAPGAETPSLRHRGQM-QPEPSTGFTATPPAPDSPQEPLVLRKFLNDSEQ 111  
 MT DS+R EAPGAE+PSLRHRG QPEP G TA+ P PDSPQEPL+LRLKFLNDSEQ

Sbjct: 1 MTAIDSIREEAPGAESPSLRHRGPSAQPEPEAGVTASTP-PDSPQEPLLLRLKFLNDSEQ 59

Query: 112 VAM-WPHDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRV 170  
VA WP DTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRV


Sbjct: 60 VARAWPQDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRV 119

Query: 171 GPPNPPCPPGSEPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLL 230  
GPP+PPCPPGSEPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLL

Sbjct: 120 GPPHPPCPPGSEPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLL 179

Query: 231 LSLLAF-MYRP 240  
LSLLAF MYRP

Sbjct: 180 LSLLAFAMYRP 190

 >gi|40807187|gb|AAH65312.1| Unknown (protein for MGC:77146) [Danio rerio]  
Length = 292

Score = 225 bits (523), Expect = 3e-57  
Identities = 136/319 (42%), Positives = 163/319 (51%), Gaps = 111/319 (34%)

Query: 2 LIEGVGDEVTVLFSV--LACLLVLALAWVSTHTAEGGDPL--PQPSGTP---TPSQ-PSM 53  
LIEGVGDEVTVLFSV L LVL LAW STHT E + L P P +P T SQ P

Sbjct: 3 LIEGVGDEVTVLFGVVFLV--LVLVLAWASTHTVKEPPEHLLSESPGASPTETDSQEP-- 58

Query: 54 MM-----TDS-----MRGE-----APGAETPS-----LRHR 74  
+ TDS +R E PG E + LRHR

Sbjct: 59 -LPPGNTDSSPGGVRDEDDKSEPGTEAGAAGQSADGSRAGGGDGGLLDDAGLGSIDGLRHR 117

Query: 75 GQM-----PE--PSTGFTATPP-----APDSPQEPLVLRKFLNDSE---QVAMWP 116  
+ PE PS AT P A D+ + +VLRKFLND+E QV P

Sbjct: 118 ---ESAGPSTHPPESTPS---ATQPSAEDAASDTHRN-MVLRKFLNDTERTAQVN---P 167

Query: 117 HDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVS---TRVGPP 173  
DTIG +KRT F G+E QVRLIYQGQLL DD+QTL SL+L N VLHCH+S TR

Sbjct: 168 QDTIGYIKRTYFAGQEHQVRLIYQGQLLQDDSQTLASLNLADNSVLHCHISQHATR---- 223

Query: 174 NPPCPPGSEPGPSG-----LEIGSLLLPLLLLLLLLLLWYCQIQYRPF--PLTAT 221  
P+G L +GSL++PL +L+L +LWY QIQYR FF P TA+

Sbjct: 224 -----AMPAGARAADQVHVALNVGSLMVPLFVLMLSVLWYFQIQYRQFF+TAPATAS 274

Query: 222 LGLAGFTLLLSLLAF-MYR 239  
L G T+ S +AF +YR

Sbjct: 275 --LVGITIFFSFVAFGVYR 291

 >gi|38091832|ref|XP\_126502.2|  RIKEN cDNA 2010008E23 [Mus musculus]  
Length = 397

Score = 158 bits (365), Expect = 4e-37  
Identities = 120/324 (37%), Positives = 161/324 (49%), Gaps = 119/324 (36%)

Query: 1 TLIEGVGDEVTVLFSVLACL-LVLALAWVSTHTAEGG-----D 37  
TLIEGVG+EV V+ V+A L L L LAW+ST+ A+ G D

Sbjct: 105 TLIEGVGNEVMVAVGVVA-LTLALVLAWLSTYVADSGNNQLLGTIVSAGDTSVLHLGHVD 163

Query: 38 PL-----PQPSG-----TPTPSQPSMMTDSMRGEA---PGAETPSLRHRG 75

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      L           P PSG           T           +DS  G+A   PGA           RG
Sbjct: 164 QLVNQGTPEPTEHPHPSGGNDDKAEET-----SDSG-GDATGEPGA-----RG 205

Query: 76 QMQPEPS-----TGFTATPP-AP----D----SPQEPLV-LRLKFLNDSEQ 111
      +M  EPS                      G  ++ P AP      D      SP      L+ +RLKFLND+E+
Sbjct: 206 EM--EPSLEHLLDIQGLPKRQAGLGSSRPEAPLGLDDGSCLSPPSLINVRLLKFLNDTEE 263

Query: 112 VAM-WPHDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRV 170
      +A+  P DT+G+LK      FPG+E Q++LIYQG+LL D  +TL SL++  NCV+HCH S
Sbjct: 264 LAVARPEDTVGTLKSKYFPGQESQMCLIYQGRLLQDPARTLSSLNITNNCVIHCHRS--- 320

Query: 171 GPPNPPCPPGSE-PGPS-----GLEIGSLLLPLLLLLLLLLLWYCQIQYRPFF- 216
      PPG+  GPS                      G+ +GSL++P+ ++LL ++WY +I YR FF
Sbjct: 321 -----PPGAAVSGPSASLTPTTEQSSLGVNVGSLMVPVEFVLLGVVWYFRINRQFFT 373

Query: 217 -PLTATLGLAGFTLLLSLLAF-MY 238
      P  AT+ L G T+  S+L F MY
Sbjct: 374 GP--ATISLVGVTVFFSILVFGMY 395

```

 >[gi|16740606|gb|AAH16187.1](#)  RIKEN cDNA 2010008E23 gene [Mus musculus]  
Length = 349

Score = 158 bits (365), Expect = 4e-37  
Identities = 120/324 (37%), Positives = 161/324 (49%), Gaps = 119/324 (36%)

```

Query: 1  TLIEGVGDEVTVLFVSLACL-LVIALAWVSTHTAEGG-----D 37
      TLIEGVG+EV V+  V+A L L L LAW+ST+ A+ G                      D
Sbjct: 57  TLIEGVGNEVMVAGVVA-LTLALVLAWLSTYVADSGNNEILGTIVSAGDTSVLHLGHVD 115

Query: 38  PL-----PQPSG-----TPTFSQPSMMMTDSMRGEA---PGAETPSLRHRG 75
      L           P PSG           T           +DS  G+A   PGA           RG
Sbjct: 116 QLVNQGTPEPTEHPHPSGGNDDKAEET-----SDSG-GDATGEPGA-----RG 157

Query: 76 QMQPEPS-----TGFTATPP-AP----D----SPQEPLV-LRLKFLNDSEQ 111
      +M  EPS                      G  ++ P AP      D      SP      L+ +RLKFLND+E+
Sbjct: 158 EM--EPSLEHLLDIQGLPKRQAGLGSSRPEAPLGLDDGSCLSPPSLINVRLLKFLNDTEE 215

Query: 112 VAM-WPHDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRV 170
      +A+  P DT+G+LK      FPG+E Q++LIYQG+LL D  +TL SL++  NCV+HCH S
Sbjct: 216 LAVARPEDTVGTLKSKYFPGQESQMCLIYQGRLLQDPARTLSSLNITNNCVIHCHRS--- 272

Query: 171 GPPNPPCPPGSE-PGPS-----GLEIGSLLLPLLLLLLLLLLWYCQIQYRPFF- 216
      PPG+  GPS                      G+ +GSL++P+ ++LL ++WY +I YR FF
Sbjct: 273 -----PPGAAVSGPSASLTPTTEQSSLGVNVGSLMVPVEFVLLGVVWYFRINRQFFT 325

Query: 217 -PLTATLGLAGFTLLLSLLAF-MY 238
      P  AT+ L G T+  S+L F MY
Sbjct: 326 GP--ATISLVGVTVFFSILVFGMY 347

```

 >[gi|20988715|gb|AAH29841.1](#)  2010008E23Rik protein [Mus musculus]  
Length = 309

Score = 158 bits (365), Expect = 4e-37  
Identities = 120/324 (37%), Positives = 161/324 (49%), Gaps = 119/324 (36%)

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Query: 1   TLIEGVGDEVTVLFSLVLAQL-LVLALAWVSTHTAEGG-----D 37
          TLIEGVG+EV V+  V+A L L L LAW+ST+ A+ G              D
Sbjct: 17  TLIEGVGNEVMVAGVVA-LTLALVLAWLSTYVADSGNNQLLGTIVSAGDT'SVHHLGHVD 75

Query: 38  PL-----PQPSG-----TPTPSQPSMMMTDSMRGEA---PGAETPSLRHRG 75
          L              P PSG              T              +DS G+A  PGA      RG
Sbjct: 76  QLVNQGTPEPTEIHPHPSGGNDDKAEET-----SDSG-GDATGEPGA-----RG 117



Query: 76  QMQPEPS-----TGFTATPP-AP-----D-----SPQEPLV-LRLKFLNDSEQ 111
          +M EPS              G ++ P AP      D      SP      L+ +RLKFLND+E+
Sbjct: 118 EM--EPSLEHLLDIQGLPKRQAGLGSSRPEAPLGLDDGSCLSPPSLINVRKFLNDTEE 175

Query: 112 VAM-WPHDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPNCVLHCHVSTRV 170
          +A+ P DT+G+LK   FPG+E Q++LIYQG+LL D  +TL SL++ NCV+HCH S
Sbjct: 176 LAVARPEDTVGTLKSKYFPGQESQMKLIYQGRLLQDPARTLSSLNITNNCVIHCHRS--- 232

Query: 171 GPPNPPCPPGSE-PGPS-----GLEIGSLLLPLLLLLLLLLLWYCQIQYRPF-- 216
          PPG+   GPS              G+ +GSL++P+ ++LL ++WY +I YR FF
Sbjct: 233 -----PPGAAVSGPSASLTPTTEQSSLGVNVGSLMVPVFVLLGVVWYFRINRYRQFFT 285

Query: 217 -PLTATLGLAGFTLLLSLLAF-MY 238
          P  AT+ L G T+  S+L F MY
Sbjct: 286 GP--ATISLVGVTVFFSILVFGMY 307

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 >gi|12842172|dbj|BAB25500.1|  unnamed protein product [Mus musculus]  
Length = 309

Score = 151 bits (350), Expect = 3e-35  
Identities = 119/324 (36%), Positives = 160/324 (49%), Gaps = 119/324 (36%)

```

Query: 1   TLIEGVGDEVTVLFSLVLAQL-LVLALAWVSTHTAEGG-----D 37
          TLIEGVG+EV V+  V+A L L L LAW+ST+ A+ G              D
Sbjct: 17  TLIEGVGNEVMVAGVVA-LTLALVLAWLSTYVADSGNNQLLGTIVSAGDT'SVLHLGHVD 75

Query: 38  PL-----PQPSG-----TPTPSQPSMMMTDSMRGEA---PGAETPSLRHRG 75
          L              P PSG              T              +DS G+A  PGA      RG
Sbjct: 76  QLVNQGTPEPTEIHPHPSGGNDDKAEET-----SDSG-GDATGEPGA-----RG 117

Query: 76  QMQPEPS-----TGFTATPP-AP-----D-----SPQEPLV-LRLKFLNDSEQ 111
          +M EPS              G ++ P AP      D      SP      L+ +RLKFLND+E+
Sbjct: 118 EM--EPSLEHLLDIQGLPKRQAGLGSSRPEAPLGLDDGSCLSPPSLINVRKFLNDTEE 175


Query: 112 VAM-WPHDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPNCVLHCHVSTRV 170
          +A+ P DT+G+LK   FPG+E Q++LIYQG+LL D  +TL SL++ NCV+HCH S
Sbjct: 176 LAVARPEDTVGTLKSKYFPGQESQMKLIYQGRLLQDPARTLSSLNITNNCVIHCHRS--- 232

Query: 171 GPPNPPCPPGSE-PGPS-----GLEIGSLLLPLLLLLLLLLLWYCQIQYRPF-- 216
          PPG+   GPS              G+ +GSL++P+ ++LL ++ Y +I YR FF
Sbjct: 233 -----PPGAAVSGPSASLTPTTEQSSLGVNVGSLMVPVFVLLGVVRYFRINRYRQFFT 285

Query: 217 -PLTATLGLAGFTLLLSLLAF-MY 238
          P  AT+ L G T+  S+L F MY
Sbjct: 286 GP--ATISLVGVTVFFSILVFGMY 307

```

 >gi|28973799|ref|NP\_803190.1|  hypothetical protein MGC3123 [Homo sapiens]

gi|21739425|emb|CAD38755.1|  hypothetical protein [Homo sapiens]  
Length = 301

Score = 151 bits (349), Expect = 4e-35

Identities = 120/326 (36%), Positives = 160/326 (49%), Gaps = 121/326 (37%)

```

Query: 1  TLIEGVGDEVTVLFSLVLAALLVLAAL--AWVSTHTAEGG----- 36
          TLIEGVG+EV V+  V+  L+LAL AW+ST+ A+ G
Sbjct: 7  TLIEGVGNEVMVAVGVVV--LILALVLAWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHV 64

Query: 37  -----DP--LPQPS-----GTPTPSQPSMMMTDSMRGEAPGA---- 66
          +P  LP PS                      G          DS  GEA GA
Sbjct: 65  DHLVAGQGNPEPTLPHPSSEGNDKAEAEAGEGRG-----DST-GEA-GAGGGV 110




Query: 67  ETPSLRH-----RGQMQLPEPSTGFTATPPAP----DS---PQEP-LV-LRLKFLND 108
          E PSL H          R      +   G +++P AP      DS   P  P L+ +RLKFLND
Sbjct: 111 E-PSLEHLLDIQGLPKR-----QAGAG-SSSPEAPLRSEDSTCLPPSPGLITVRLKFLND 163

Query: 109 SEQVAM-WPHDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTIGSLHLPPNCVLHCHVS 167
          +E++A+  P DT+G+LK   FPG+E Q++LIYQG+LL D  +TL SL++  NCV+HCH S
Sbjct: 164 TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTLRSLNITDNCVIHCHRS 223

Query: 168 TRVGPPNPPCPPGSE-PGPS-----GLEIGSLLLPLLLLLLLLLLWYCQIQYR 213
          PPGS  PGPS                      G+ +GSL++P+ ++LL ++WY +I YR
Sbjct: 224 -----PPGSAVPGPSASLAPSATEPPRLGVNVGSLMVPVFVLLGVVWYFRINYR 273

Query: 214 PFFPLTATLGLAGFTLLLSLLAF-MY 238
          FF  AT+ L G T+  S L F MY
Sbjct: 274 QFFTAPATVSLVGVTVFFSFLVFGMY 299

```

gi|33341676|gb|AAQ15209.1|  FP2653 [Homo sapiens]  
gi|37182679|gb|AAQ89140.1|  ELSD1897 [Homo sapiens]  
gi|39645315|gb|AAH63489.1|  MGC3123 protein [Homo sapiens]  
Length = 301

Score = 151 bits (349), Expect = 4e-35

Identities = 120/326 (36%), Positives = 160/326 (49%), Gaps = 121/326 (37%)

```

Query: 1  TLIEGVGDEVTVLFSLVLAALLVLAAL--AWVSTHTAEGG----- 36
          TLIEGVG+EV V+  V+  L+LAL AW+ST+ A+ G
Sbjct: 7  TLIEGVGNEVMVAVGVVV--LILALVLAWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHV 64

Query: 37  -----DP--LPQPS-----GTPTPSQPSMMMTDSMRGEAPGA---- 66
          +P  LP PS                      G          DS  GEA GA
Sbjct: 65  DHLVAGQGNPEPTLPHPSSEGNDKAEAEAGEGRG-----DST-GEA-GAGGGV 110

Query: 67  ETPSLRH-----RGQMQLPEPSTGFTATPPAP----DS---PQEP-LV-LRLKFLND 108
          E PSL H          R      +   G +++P AP      DS   P  P L+ +RLKFLND
Sbjct: 111 E-PSLEHLLDIQGLPKR-----QAGAG-SSSPEAPLRSEDSTCLPPSPGLITVRLKFLND 163



Query: 109 SEQVAM-WPHDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTIGSLHLPPNCVLHCHVS 167
          +E++A+  P DT+G+LK   FPG+E Q++LIYQG+LL D  +TL SL++  NCV+HCH S
Sbjct: 164 TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTLRSLNITDNCVIHCHRS 223

Query: 168 TRVGPPNPPCPPGSE-PGPS-----GLEIGSLLLPLLLLLLLLLLWYCQIQYR 213
          PPGS  PGPS                      G+ +GSL++P+ ++LL ++WY +I YR
Sbjct: 224 -----PPGSAVPGPSASLAPSATEPPSLGVNVGSLMVPVFVLLGVVWYFRINYR 273

```



Query: 214 PFFPLTATLGLAGFTLLLSLLAF-MY 238  
 FF AT+ L G T+ S L F MY  
 Sbjct: 274 QFFTAPATVSLVGVTVFFSFLVFGMY 299

 >gi|27689889|ref|XP\_221010.1|  similar to RIKEN cDNA 2010008E23 gene [Rattus no  
 Length = 355

Score = 144 bits (333), Expect = 5e-33  
 Identities = 115/323 (35%), Positives = 152/323 (47%), Gaps = 117/323 (36%)

Query: 1 TLIEGVGDEVTVLFSV--LACLLVLALAWVSTHTAEGG----- 36  
 TLIEGVG+EV V+ V L L L LAW+ST+ A+  
 Sbjct: 63 TLIEGVGNEVMVAGVVVLT---LALVLAWLSTYVADSSNSQLLGTIVSAGDTSVLHLGHIV 120


Query: 37 DPL-----PQPSG-----TPTPSQPSMMMTDS---MRGEAPGAETPSLRHR 74  
 D L P PSG T +DS GE PGA R  
 Sbjct: 121 DQLVNQGTPEPTEHPHPSGGSDDKAEET-----SDSGGDTTGE-PGA-----R 162

Query: 75 GQMQPEPS-----TGFTATPPAP-----DS----PQEPLV-LRLKFLNDSE 110  
 G M EPS G ++ P DS P L+ +RLKFLND+E  
 Sbjct: 163 GDM--EPSLEHLLDIQGLPKRQAGLSSSRPEASLGLDDSTCLSPSPSLINVRLKFLNDTE 220

Query: 111 QVAM-WPHDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTR 169  
 ++A+ P DT+G+LK FPG+E Q++LIYQG+LL D +TL SL++ NCV+HCH S  
 Sbjct: 221 ELAVARPEDTVGTLKSKYFPGQESQMKLIYQGRLLQDPARTLSSLNITNNCVHCHRS-- 278

Query: 170 VGPPNPPCPPGSE-PGPS-----GLEIGSLLLPLLLLLLLLLLWYCQIQYRPF 216  
 PPG+ GPS G+ +GSL++P+ ++LL ++WY +I YR FF  
 Sbjct: 279 -----PPGAAVSGPSTSIPTTEQSSSLGVNVGSLMVPVFVLLGVVWYFRINRQFF 330

Query: 217 PLTATLGLAGFTLLLSLLAF-MY 238  
 AT+ L G T+ S L F MY  
 Sbjct: 331 TAPATVSLVGVTVFFSFLVFGMY 353

 >gi|22204247|emb|CAD43429.1| SI:dZ180G5.5 (novel ubiquitin) [Danio rerio]  
 Length = 291

Score = 108 bits (249), Expect = 2e-22  
 Identities = 68/159 (42%), Positives = 89/159 (55%), Gaps = 33/159 (20%)

Query: 102 RLKFLNDSEQVA-MWPHDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQ-TLGSLHLPPN 159  
 RLKFLND+E++A + P DTIG LK F GRE Q++LIYQGQLL D Q +L SL++ N  
 Sbjct: 140 RLKFLNDTEEIAVLRPQDTIGLLKSKYFSGREHQIKLIYQGQLL-QDPQRSLLSLNITHN 198

Query: 160 CVLHCHVS----TRVGPPNPPCPPGSEPGP-----SG-----LEIGSLLLPLLL 199  
 VLHCH+S R +E GP SG L G L++P+ +  
 Sbjct: 199 SVLHCHISQAQAQR-----EAAEDGPRASRVSILSGGLRSAGVALSTGGLVIPVFV 249

Query: 200 LLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAF-M 237  
 +LL ++WY +I YR F AT+ L G T+ S L F M  
 Sbjct: 250 VLLAVVWYFRINRQLEFAPATISLVGVTVFFSFLIFGM 288